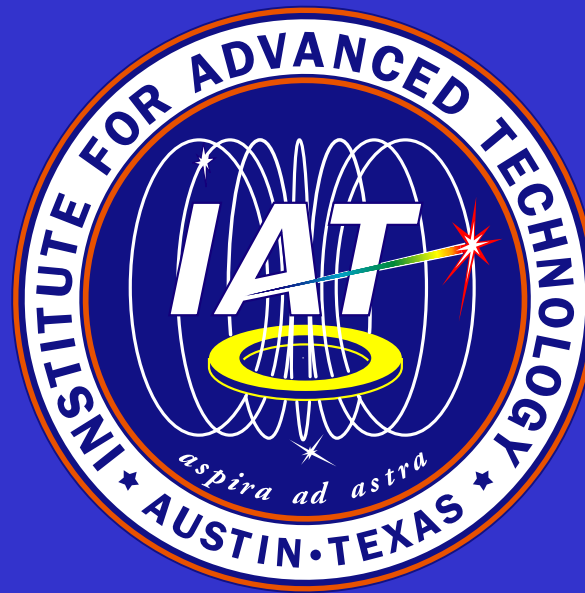


The Army's University Affiliated Research Center

The UTEXAS UARC

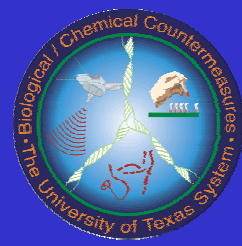
Chem-Bio Program Objectives



Dr. Steve Kornguth, Director

Biological and Chemical (B/C) Countermeasures

Report Documentation Page				Form Approved OMB No. 0704-0188	
Public reporting burden for the collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington VA 22202-4302. Respondents should be aware that notwithstanding any other provision of law, no person shall be subject to a penalty for failing to comply with a collection of information if it does not display a currently valid OMB control number.					
1. REPORT DATE 18 NOV 2003		2. REPORT TYPE N/A		3. DATES COVERED -	
4. TITLE AND SUBTITLE The UTEXAS UARC Chem-Bio Program Objectives				5a. CONTRACT NUMBER	
				5b. GRANT NUMBER	
				5c. PROGRAM ELEMENT NUMBER	
6. AUTHOR(S)				5d. PROJECT NUMBER	
				5e. TASK NUMBER	
				5f. WORK UNIT NUMBER	
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Institute for Advanced Technology, UT Austin				8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)				10. SPONSOR/MONITOR'S ACRONYM(S)	
				11. SPONSOR/MONITOR'S REPORT NUMBER(S)	
12. DISTRIBUTION/AVAILABILITY STATEMENT Approved for public release, distribution unlimited					
13. SUPPLEMENTARY NOTES See also ADM001851, Proceedings of the 2003 Joint Service Scientific Conference on Chemical & Biological Defense Research, 17-20 November 2003. , The original document contains color images.					
14. ABSTRACT					
15. SUBJECT TERMS					
16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT UU	18. NUMBER OF PAGES 18	19a. NAME OF RESPONSIBLE PERSON
a. REPORT unclassified	b. ABSTRACT unclassified	c. THIS PAGE unclassified			



Simultaneous Detection of Multiple Pathogenicity Islands (PI)

Dr. Shelley Payne, UT Austin

Dr. Kerry Oliver, Radix BioSolutions, Ltd.

Dr. James J. Valdes, Edgewood Chemical Biological Command

Dr. Steve Kornguth, Dr. Robert C. Chin*, Institute for Advanced Technology, UT Austin

Goal

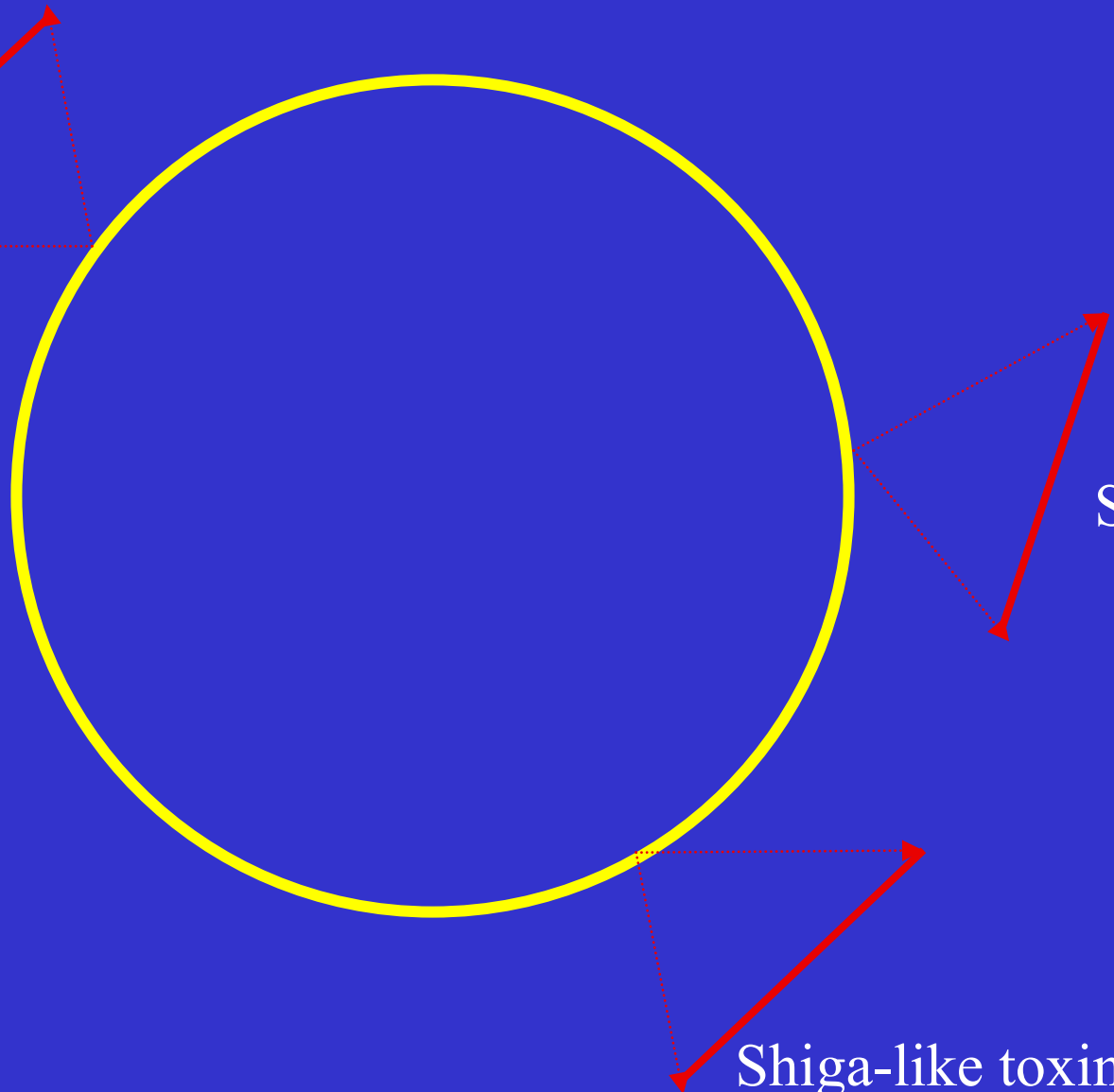
- Characterize pathogenicity islands, DNA factors present in virulent strains but absent from closely related, avirulent strains of bacteria
- Transition UT pathogenicity island technology to rapid commercial screening platform

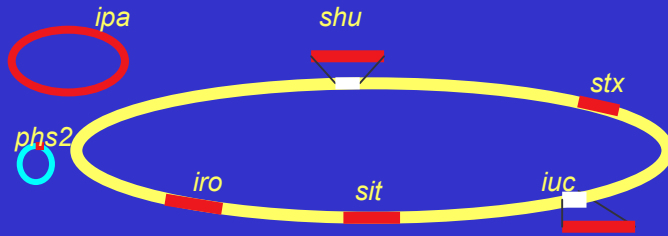
E. coli O157:H7

LEE

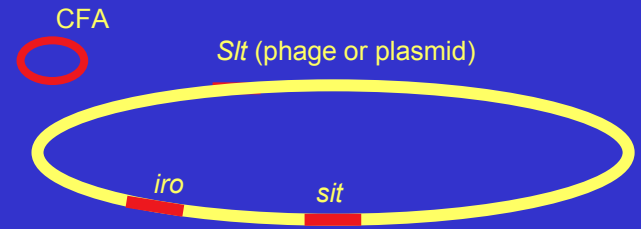
Shu

Shiga-like toxin



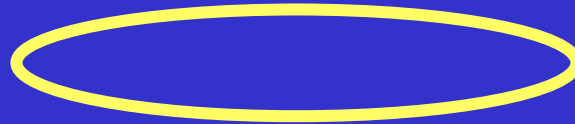


Shigella/EIEC

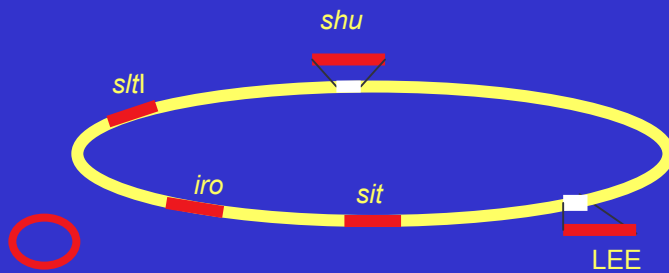


E. coli ETEC

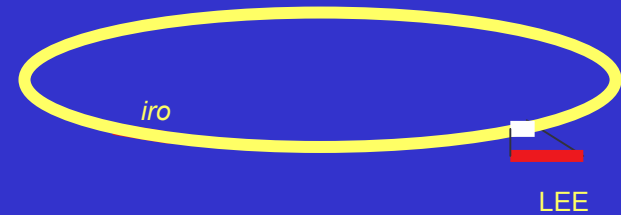
non-pathogenic *E. coli*



E. coli O157:H7



E. coli EPEC



General Characteristics of a rapid screening platform

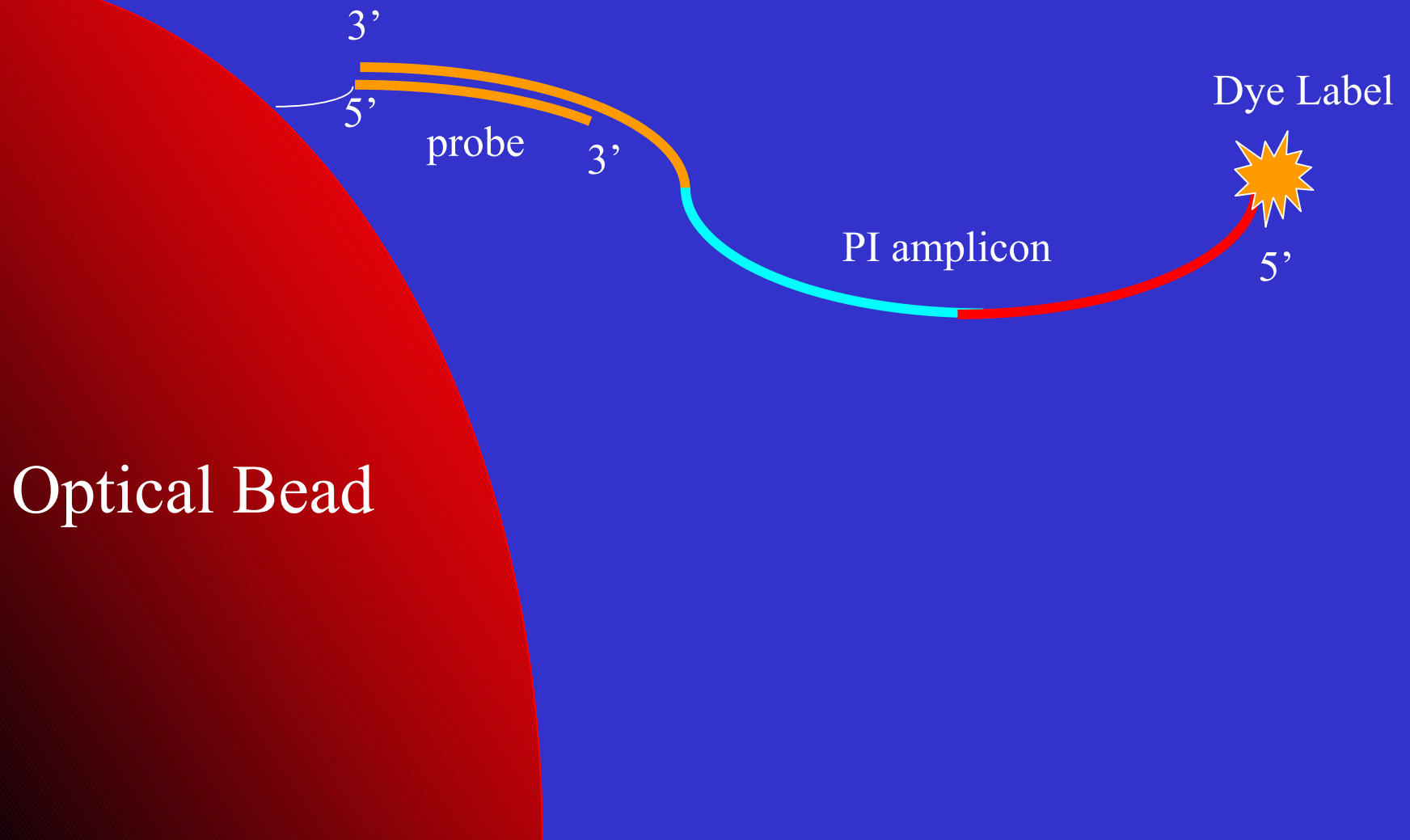
- Flexible
- Reproducible
- Simple
- Stable
- Minimize false positives and negatives

Pathogenicity Island

Multiplexing

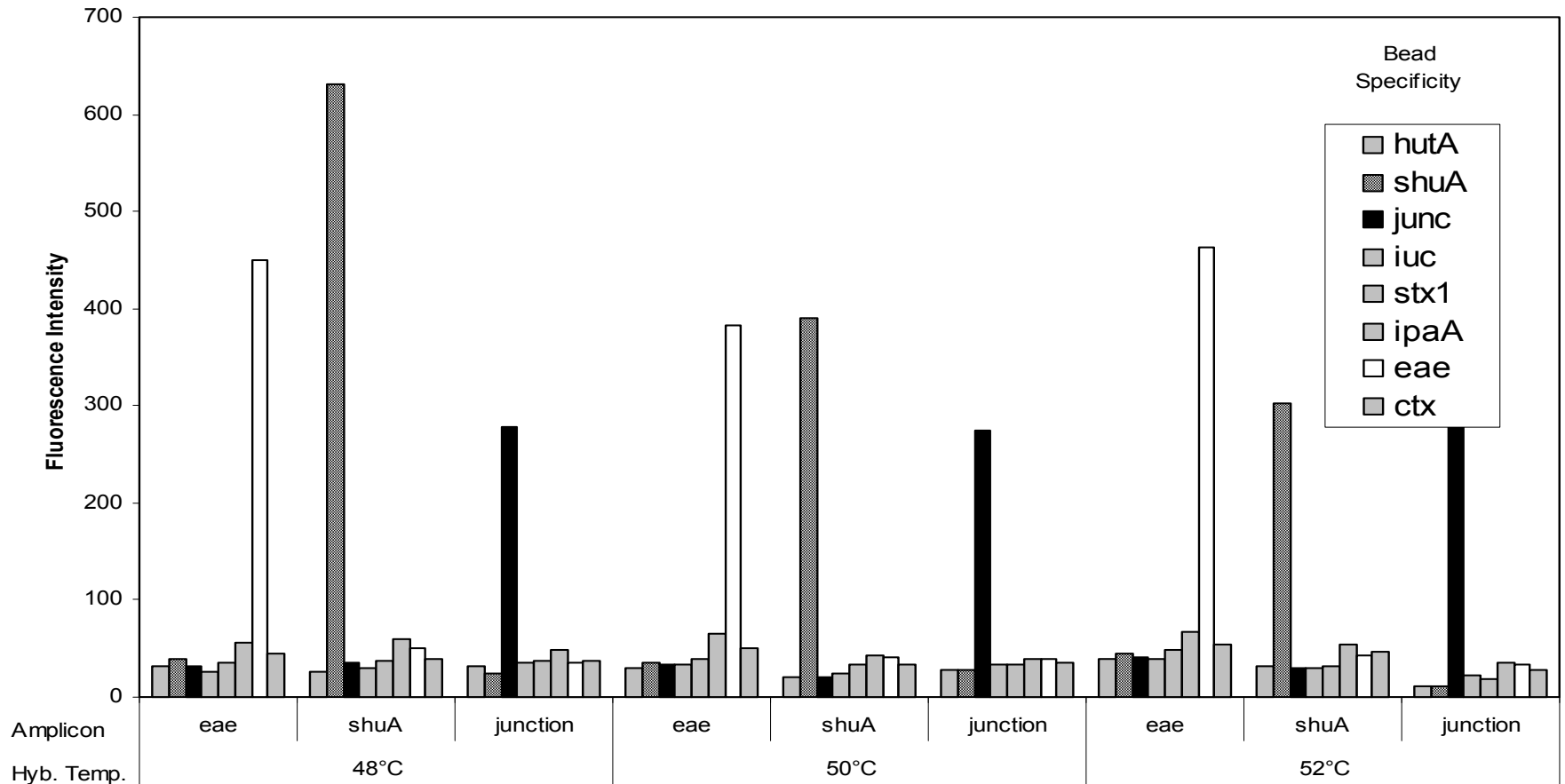
- Identify pathogenic properties rather than specific organisms
- Pattern identification of pathogens
- As new factors can be rapidly added to current stocks
- Multiple sequences for each factor can essentially eliminate false positives and false negatives

Pathogenicity Island Assay Format



IAT/Radix Pathogenicity Island Multiplexing Assay

Temperature study

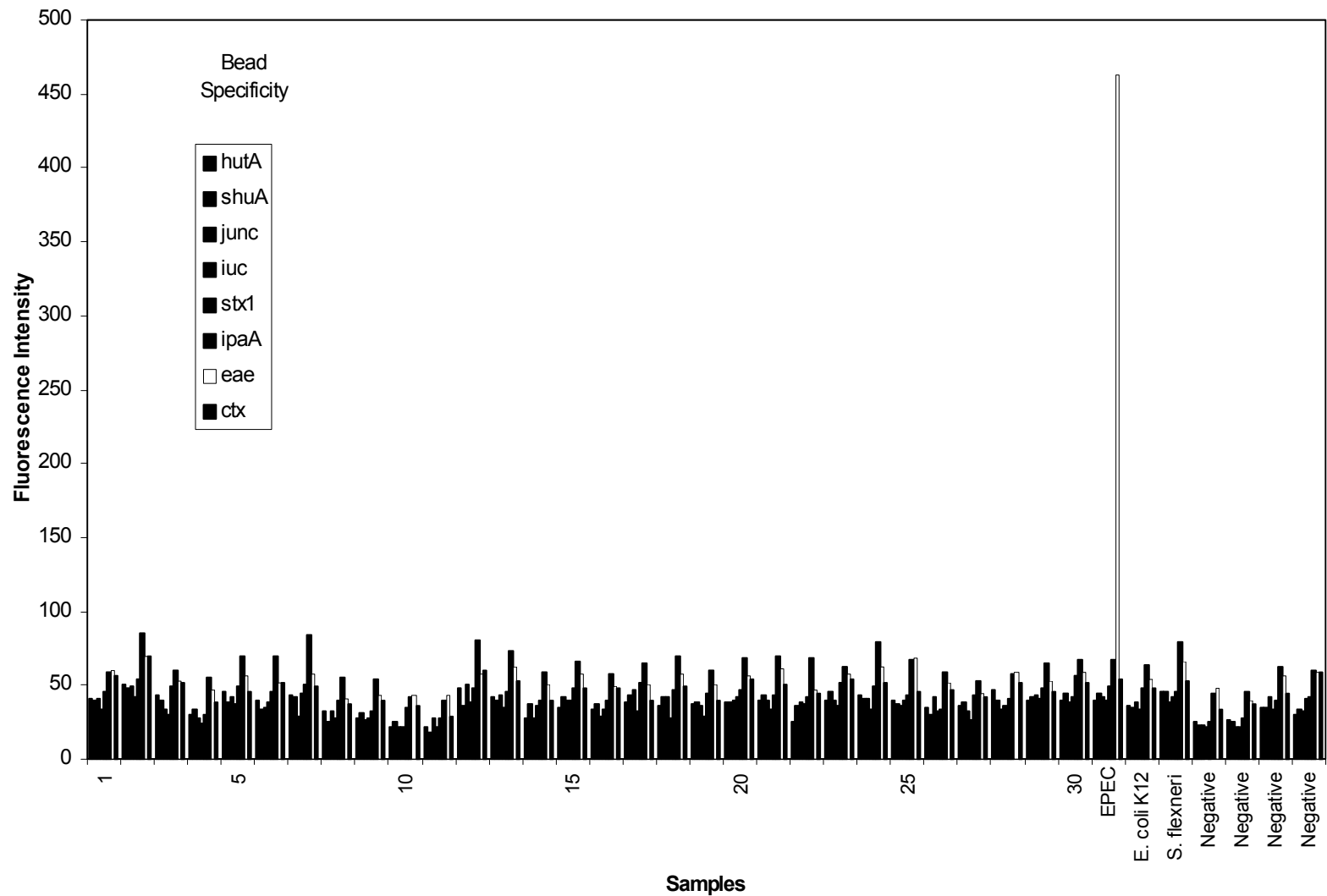


Are Pathogenicity Islands Ubiquitously Distributed in the Environment?

- 30 Dormitory rooms sampled
 - Surface swabbed (3 surfaces per room)
 - Inoculated into broth
- Amplified with 4 different PI primer sets
- Hybridized with 8 different probes at 52°C

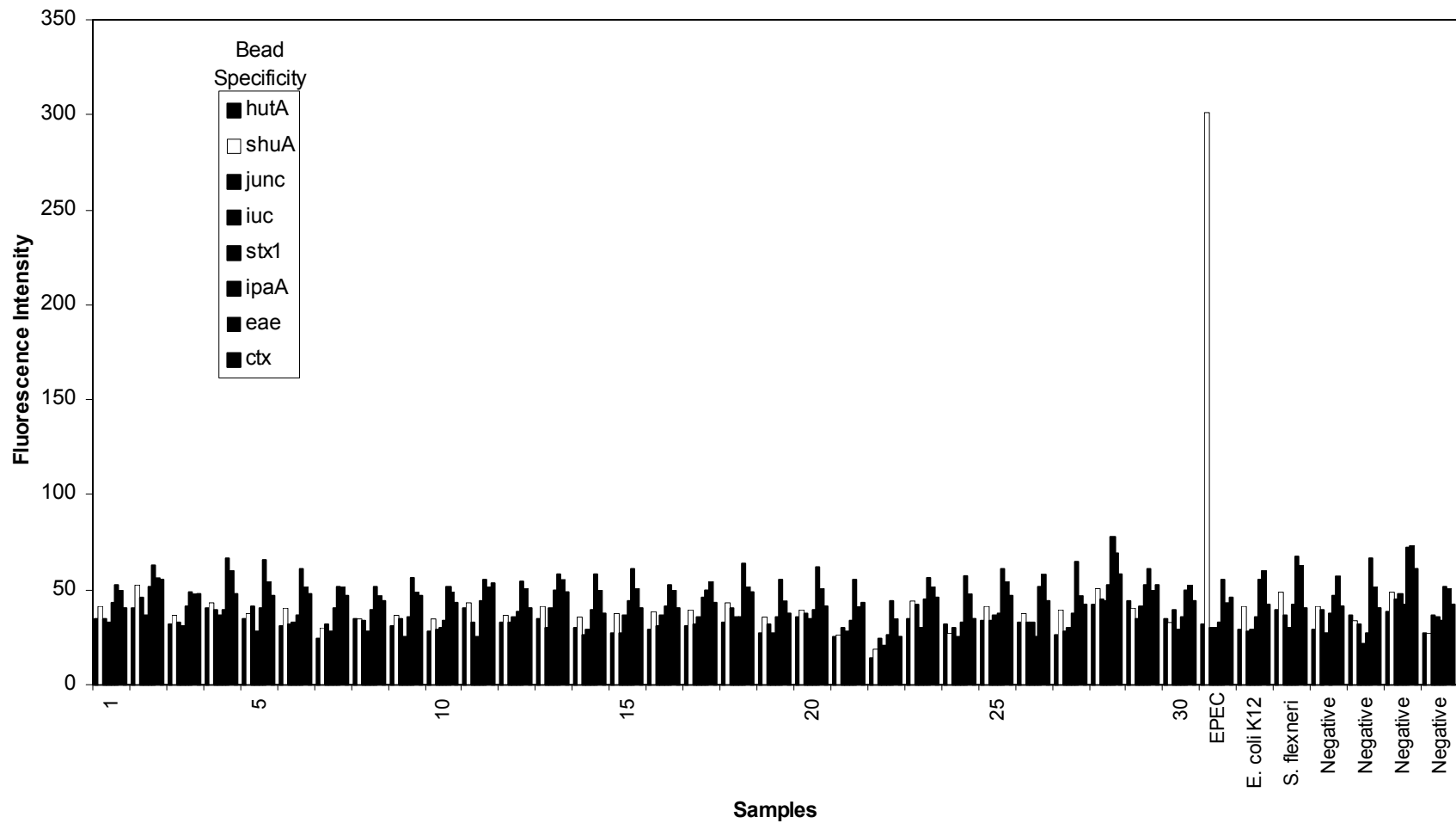
30 Dormitory room samples

eae amplification

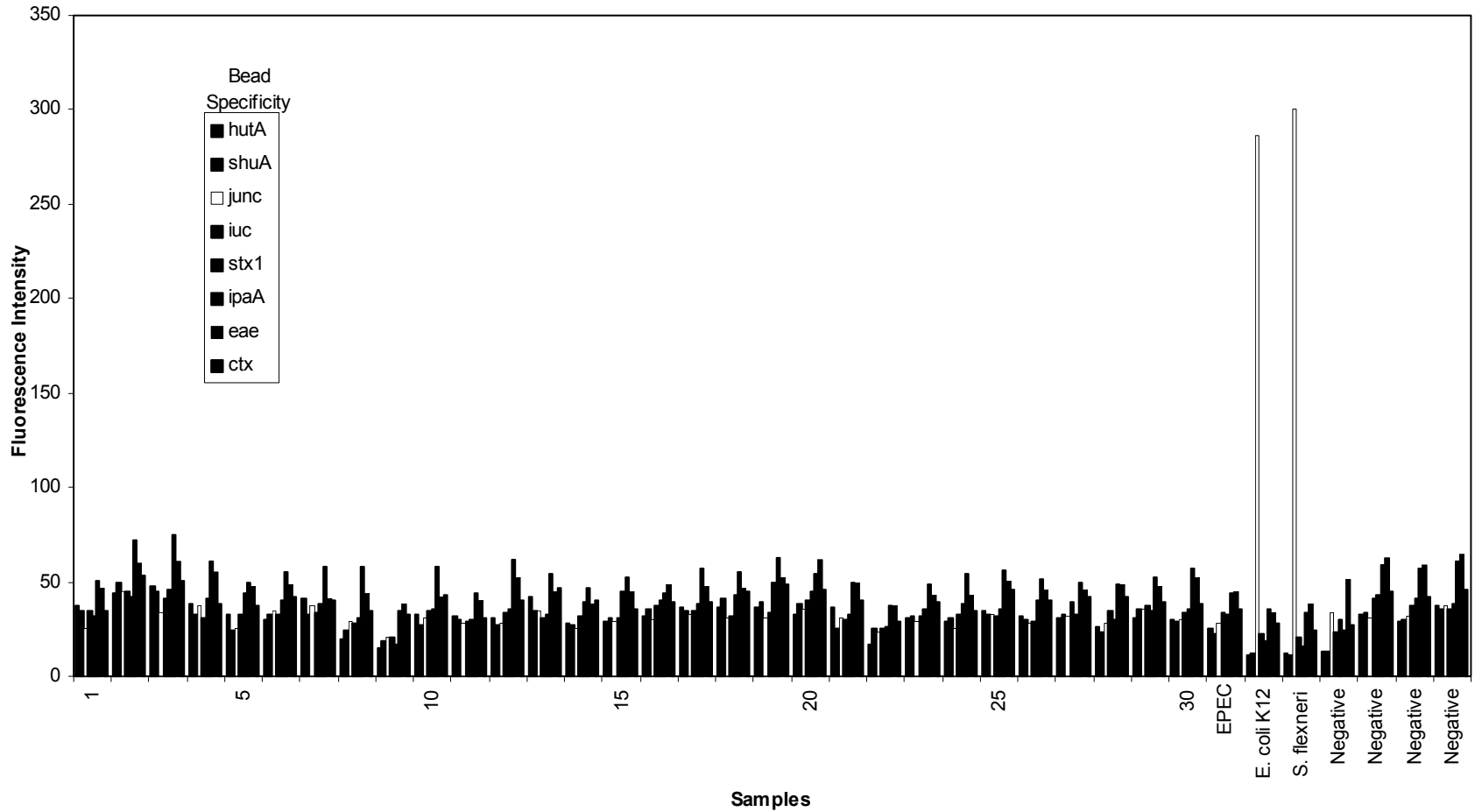


30 Dormitory room samples

Shu amplification

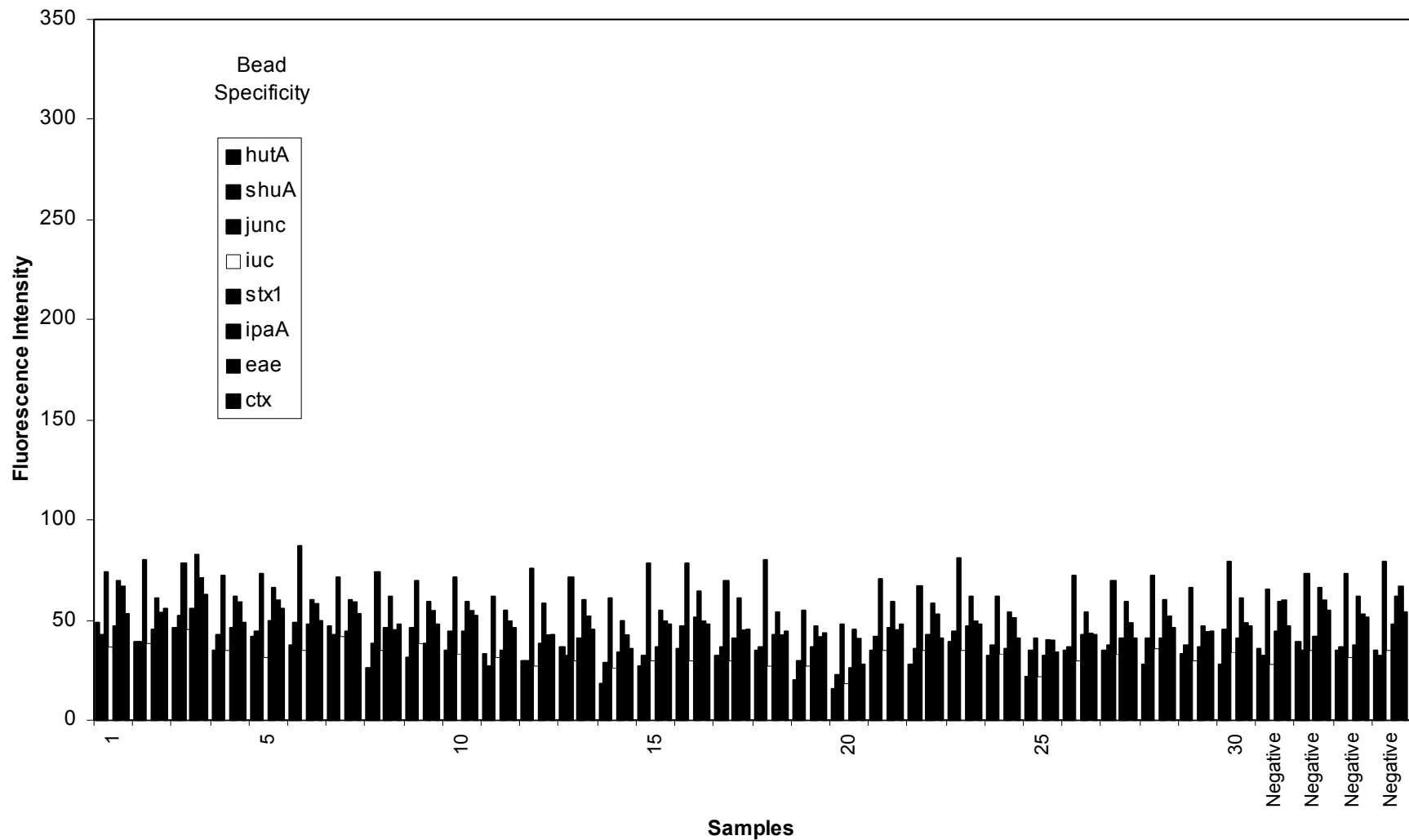


30 Dormitory room samples junction amplification

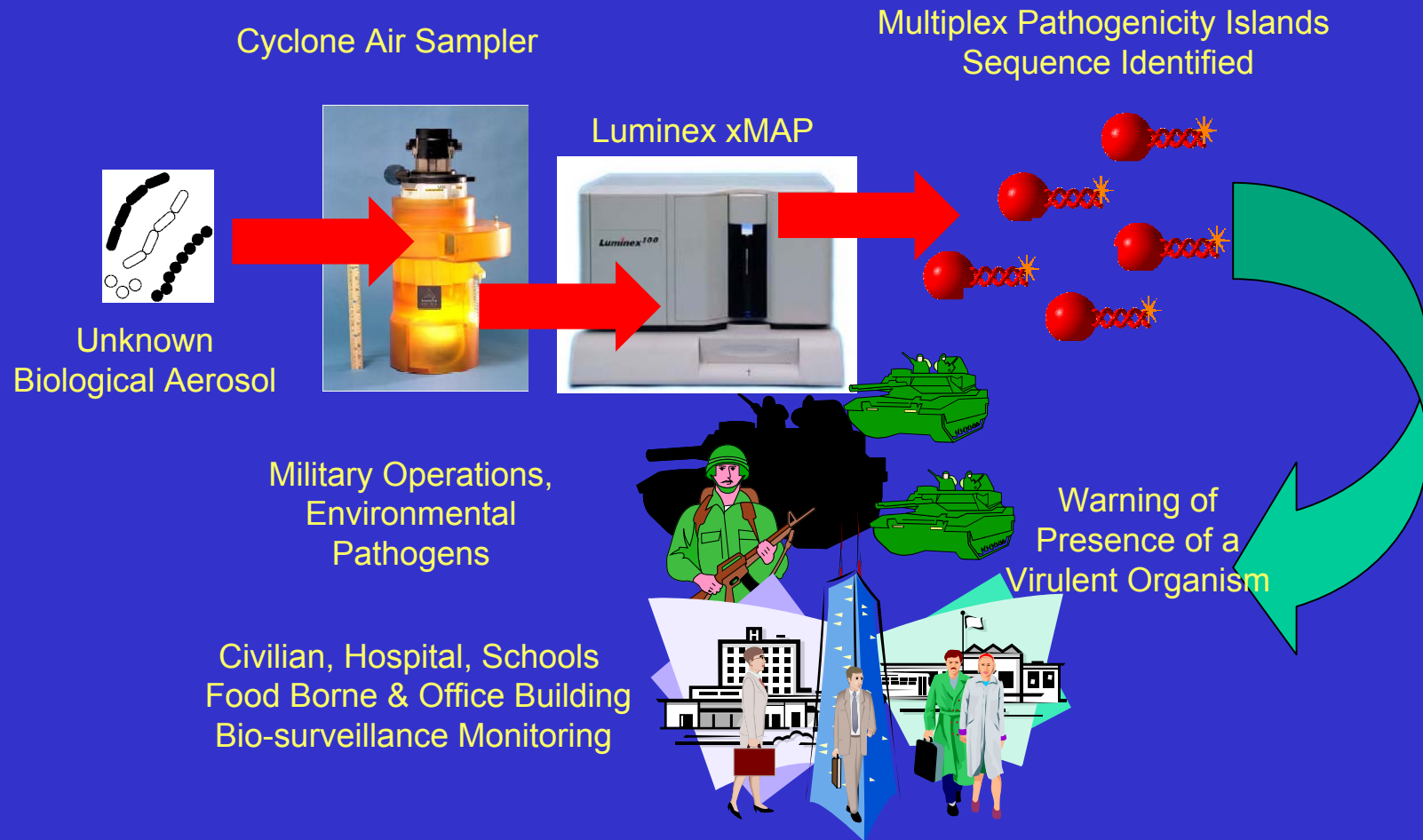


30 Dormitory room samples

iuc amplification



UT-Radix Detection/Identification Platform



Conclusions

- Probes have been designed to hybridize to specific PI sequences
- The PI assay has good sensitivity
- No genomic sequences for pathogens are detected in dormitory environments, therefore pathogens are NOT distributed ubiquitously in such environments

Future Plans

- Optimize probe design to eliminate cross-reactivity thus eliminating false positives and false negatives
- Optimize amplicon design needs to be undertaken to eliminate steric effects in the assay design
- Determine maximum PI amplicons that can be simultaneously screened

THE UNIVERSITY OF TEXAS COMPONENT

